

Query Match 100.0%; Score 7; DB 11; Length 295;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKRILHC 7
 |||||
 Db 274 KKRILHC 280

RESULT 2

ID Q9BRW8 PRELIMINARY; PRT; 296 AA.
 AC Q9BRW8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE SIMILAR TO BILIVERDIN REDUCTASE A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005902; AAH05902.1;
 SQ SEQUENCE 296 AA; 33432 MW; A389AFDDB6ADBBF CRC64;

Query Match 100.0%; Score 7; DB 4; Length 296;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKRILHC 7
 |||||
 Db 275 KKRILHC 281

RESULT 3

ID Q9DD21 PRELIMINARY; PRT; 303 AA.
 AC Q9DD21;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 0610006A11RIK PROTEIN.
 GN 0610006A11RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
 RX MEDLINE=21083660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Saki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyszaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK002231; BAB21950.1;
 DR MGD; MGI:1915580; 0610006A11RIK.
 DR InterPro; IPR000683; GFO_IDH_MoCA.
 DR Pfam; PF01408; GFO_IDH_MoCA; 1.
 SQ SEQUENCE 303 AA; 34491 MW; 52D8A3B02EE956EB CRC64;

Query Match 100.0%; Score 7; DB 11; Length 303;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKRILHC 7
 |||||
 Db 274 KKRILHC 280

RESULT 4

ID Q32948 PRELIMINARY; PRT; 42 AA.
 AC Q32948;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE ORF42A.
 GN PSAM.
 OS Pinus thunbergii (Green pine) (Japanese black pine).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92212283; PubMed=1557027;
 RA Tsudzuki J., Nakashima K., Tsudzuki T., Hiratsuka J., Shibata M.,
 RA Wakasugi T., Sugiura M.;
 RT "Chloroplast DNA of black pine retains a residual inverted repeat
 RT lacking rRNA genes: nucleotide sequences of trnQ, trnK, psbA, trnI and
 RT trnH and the absence of rps16.";
 RL Mol. Gen. Genet. 232:206-214(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95094312; PubMed=8001170;
 RA Tsudzuki J., Ito S., Tsudzuki T., Wakasugi T., Sugiura M.;
 RT "A new gene encoding tRNA(Pro) (GGG) is present in the chloroplast
 RT genome of black pine: a compilation of 32 tRNA genes from black pine
 RT chloroplasts.";
 RL Curr. Genet. 26:153-158(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95024047; PubMed=7937893;
 RA Wakasugi T., Tsudzuki J., Ito S., Nakashima K., Tsudzuki T.,
 RA Sugiura M.;
 RT "Loss of all ndh genes as determined by sequencing the entire
 RT chloroplast genome of the black pine Pinus thunbergii.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9794-9798(1994).
 DR EMBL; D17510; BAA04352.1;
 KW Chloroplast.
 SQ SEQUENCE 42 AA; 4972 MW; 9B06BE464A5F8565 CRC64;

Query Match 85.7%; Score 6; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 5.8;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKRILH 6
 |||||
 Db 30 KKRILH 35